Validated By CRFValidator v 1.0.3

Application No: 10814752   Version No: 2.0

Input Set:

Output Set:

Started: 2008-07-25 21:55:49.943
Finished: 2008-07-25 21:56:02.466
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 523 ms
Total Warnings: 13
Total Errors: 0
No. of SeqIDs Defined: 34
Actual SeqID Count: 34

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<110> DeAngelis, Paul

<120> HEPARIN/HEPAROSAN SYNTHASE FROM P. MULTOCIDA, SOLUBLE AND SINGLE
       ACTION CATALYSTS THEREOF AND METHODS OF MAKING AND USING SAME

<130> 4599.014

<140> 10814752
<141> 2004-03-31

<150> 60/458,939
<151> 2003-03-31

<150> 10/142,143
<151> 2002-05-08

<150> 60/289,554
<151> 2001-05-08

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<151> 2001-06-06

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<170> PatentIn version 3.4

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<213> Pasteurella multocida

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gatatatgta aaaaaaatat aacacaatca aaaagtaata aaatagaaga agataatatt   180

tctggagaaa acaaattttc agtatcaata aaagatctat ataacgaaat aagcaatagt   240

gaattaggga ttacaaaaga aagactagga gcccccccctc tagtcagtat tataatgact   300

tctcataata cagaaaaatt cattgaagcc tcaattaatt cactattatt gcaaacatac   360

aataacttag aagttatcgt tgtagatgat tatagcacag ataaaacatt tcagatcgca   420

tccagaatag caaactctac aagtaaagta aaaacattcc gattaaactc aaatctaggg   480

acatactttg cgaaaaatac aggaattttta aagtctaaag gagatattat tttctttcag   540

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ataataaaag ttaatgataa taaatacaaa ttaggattaa taactttagg cgtttataga      720

aaagtattta atgaaattgg ttttttaac tgcacaacca aagcatcgga tgatgaattt      780

tatcatagaa taattaaata ctatggtaaa aataggataa ataacttatt ctaccactg      840

tattataaca caatgcgtga agattcatta ttttctgata tggttgagtg ggtagatgaa      900

aataatataa agcaaaaaac ctctgatgct agacaaaatt atctccatga attccaaaaa      960

atacacaatg aaaggaaatt aaatgaatta aaagagattt ttagctttcc tagaattcat     1020

gacgccttac ctatatcaaa agaaatgagt aagctcagca accctaaaat tcctgtttat     1080

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aaaaaccaat gcgatcattt tcatatttat cttgatggat atccagaagt acctgatttt     1200

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tatataactt gtgatgatga tatccggtat cctgctgact acacaaacac tatgataaaa     1380

aaaattaata aatacaatga taaagcagca attggattac atggtgttat attcccaagt     1440

agagtcaaca agtattttttc atcagacaga attgtctata attttcaaaa acctttagaa     1500

aatgatactg ctgtaaatat attaggaact ggaactgttg cctttagagt atctattttt     1560

aataaatttt ctctatctga ttttgagcat cctggcatgg tagatatcta ttttttctata     1620

ctatgtaaga aaaacaatat actccaagtt tgtatatcac gaccatcgaa ttggctaaca     1680

gaagataaca aaaacactga gaccttattt catgaattcc aaaatagaga tgaaatacaa     1740

agtaaactca ttatttcaaa caacccttgg ggatactcaa gtatatatcc actattaaat     1800

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Glu Ser Leu Val Lys Tyr Asn Ile Asp Ile Cys Lys Lys Asn Ile Thr
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Gln Ser Lys Ser Asn Lys Ile Glu Glu Asp Asn Ile Ser Gly Glu Asn
         50                  55                  60


Lys Phe Ser Val Ser Ile Lys Asp Leu Tyr Asn Glu Ile Ser Asn Ser
65                  70                  75                  80


Glu Leu Gly Ile Thr Lys Glu Arg Leu Gly Ala Pro Pro Leu Val Ser
                  85                  90                  95


Ile Ile Met Thr Ser His Asn Thr Glu Lys Phe Ile Glu Ala Ser Ile
              100                 105                 110


Asn Ser Leu Leu Leu Gln Thr Tyr Asn Asn Leu Glu Val Ile Val Val
         115                 120                 125


Asp Asp Tyr Ser Thr Asp Lys Thr Phe Gln Ile Ala Ser Arg Ile Ala
         130                 135                 140


Asn Ser Thr Ser Lys Val Lys Thr Phe Arg Leu Asn Ser Asn Leu Gly
145                 150                 155                 160


Thr Tyr Phe Ala Lys Asn Thr Gly Ile Leu Lys Ser Lys Gly Asp Ile
                  165                 170                 175


Ile Phe Phe Gln Asp Ser Asp Asp Val Cys His His Glu Arg Ile Glu
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Arg Cys Val Asn Ala Leu Leu Ser Asn Lys Asp Asn Ile Ala Val Arg
         195                 200                 205


Cys Ala Tyr Ser Arg Ile Asn Leu Glu Thr Gln Asn Ile Ile Lys Val
         210                 215                 220


Asn Asp Asn Lys Tyr Lys Leu Gly Leu Ile Thr Leu Gly Val Tyr Arg
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Lys Val Phe Asn Glu Ile Gly Phe Phe Asn Cys Thr Thr Lys Ala Ser
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Asp Asp Glu Phe Tyr His Arg Ile Ile Lys Tyr Tyr Gly Lys Asn Arg
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Ser Leu Phe Ser Asp Met Val Glu Trp Val Asp Glu Asn Asn Ile Lys
        290                      295                  300


Gln Lys Thr Ser Asp Ala Arg Gln Asn Tyr Leu His Glu Phe Gln Lys
305                      310                  315                  320


Ile His Asn Glu Arg Lys Leu Asn Glu Leu Lys Glu Ile Phe Ser Phe
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Pro Arg Ile His Asp Ala Leu Pro Ile Ser Lys Glu Met Ser Lys Leu
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Ser Asn Pro Lys Ile Pro Val Tyr Ile Asn Ile Cys Ser Ile Pro Ser
        355                      360                  365


Arg Ile Lys Gln Leu Gln Tyr Thr Ile Gly Val Leu Lys Asn Gln Cys
        370                      375                  380


Asp His Phe His Ile Tyr Leu Asp Gly Tyr Pro Glu Val Pro Asp Phe
385                      390                  395                  400


Ile Lys Lys Leu Gly Asn Lys Ala Thr Val Ile Asn Cys Gln Asn Lys
                405                      410                  415


Asn Glu Ser Ile Arg Asp Asn Gly Lys Phe Ile Leu Leu Glu Lys Leu
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Ile Lys Glu Asn Lys Asp Gly Tyr Tyr Ile Thr Cys Asp Asp Ile
        435                      440                  445


Arg Tyr Pro Ala Asp Tyr Thr Asn Thr Met Ile Lys Lys Ile Asn Lys
        450                      455                  460


Tyr Asn Asp Lys Ala Ala Ile Gly Leu His Gly Val Ile Phe Pro Ser
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Arg Val Asn Lys Tyr Phe Ser Ser Asp Arg Ile Val Tyr Asn Phe Gln
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Lys Pro Leu Glu Asn Asp Thr Ala Val Asn Ile Leu Gly Thr Gly Thr
                500   505   510

Val Ala Phe Arg Val Ser Ile Phe Asn Lys Phe Ser Leu Ser Asp Phe
        515   520   525

Glu His Pro Gly Met Val Asp Ile Tyr Phe Ser Ile Leu Cys Lys Lys
        530   535   540

Asn Asn Ile Leu Gln Val Cys Ile Ser Arg Pro Ser Asn Trp Leu Thr
545   550   555   560

Glu Asp Asn Lys Asn Thr Glu Thr Leu Phe His Glu Phe Gln Asn Arg
                565   570   575

Asp Glu Ile Gln Ser Lys Leu Ile Ile Ser Asn Asn Pro Trp Gly Tyr
                580   585   590

Ser Ser Ile Tyr Pro Leu Leu Asn Asn Asn Ala Asn Tyr Ser Glu Leu
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Ile Pro Cys Leu Ser Phe Tyr Asn Glu
        610   615

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<211>   1854
<212>   DNA
<213>   Pasteurella multocida

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gatatatgta aaaaaaatat aacacaatca aaaagtaata aaatagaaga agataatatt   180

tctggagaaa acaaattttc agtatcaata aaagatctat ataacgaaat aagcaatagt   240

gaattaggga ttacaaaaga aagactagga gcccccccctc tagtcagtat tataatgact   300

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tccagaatag caaactctac aagtaaagta aaaacattcc gattaaactc aaatctaggg   480

acatactttg cgaaaaatac aggaatttta aagtctaaag gagatattat tttctttcag   540

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aataatataa agcaaaaaac ctctgatgct agacaaaatt atctccatga attccaaaaa   960

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            20                  25                  30


Glu Ser Leu Val Lys Tyr Asn Ile Asp Ile Cys Lys Lys Asn Ile Thr
        35                  40                  45


Gln Ser Lys Ser Asn Lys Ile Glu Glu Asp Asn Ile Ser Gly Glu Asn
    50                  55                  60


Lys Phe Ser Val Ser Ile Lys Asp Leu Tyr Asn Glu Ile Ser Asn Ser
65                  70                  75                  80


Glu Leu Gly Ile Thr Lys Glu Arg Leu Gly Ala Pro Pro Leu Val Ser
            85                  90                  95


Ile Ile Met Thr Ser His Asn Thr Glu Lys Phe Ile Glu Ala Ser Ile
            100                 105                 110


Asn Ser Leu Leu Leu Gln Thr Tyr Asn Asn Leu Glu Val Ile Val Val
        115                 120                 125


Asp Asp Tyr Ser Thr Asp Lys Thr Phe Gln Ile Ala Ser Arg Ile Ala
    130                 135                 140


Asn Ser Thr Ser Lys Val Lys Thr Phe Arg Leu Asn Ser Asn Leu Gly
145                 150                 155                 160


Thr Tyr Phe Ala Lys Asn Thr Gly Ile Leu Lys Ser Lys Gly Asp Ile
            165                 170                 175


Ile Phe Phe Gln Asp Ser Asp Asp Val Cys His His Glu Arg Ile Glu
            180                 185                 190


Arg Cys Val Asn Ala Leu Leu Ser Asn Lys Asp Asn Ile Ala Val Arg
        195                 200                 205


Cys Ala Tyr Ser Arg Ile Asn Leu Glu Thr Gln Asn Ile Ile Lys Val
    210                 215                 220


Asn Asp Asn Lys Tyr Lys Leu Gly Leu Ile Thr Leu Gly Val Tyr Arg
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Lys Val Phe Asn Glu Ile Gly Phe Phe Asn Cys Thr Thr Lys Ala Ser
                   245   250   255

Asp Asp Glu Phe Tyr His Arg Ile Ile Lys Tyr Tyr Gly Lys Asn Arg
                   260   265   270

Ile Asn Asn Leu Phe Leu Pro Leu Tyr Tyr Asn Thr Met Arg Glu Asp
                   275   280   285

Ser Leu Phe Ser Asp Met Val Glu Trp Val Asp Glu Asn Asn Ile Lys
         290   295   300

Gln Lys Thr Ser Asp Ala Arg Gln Asn Tyr Leu His Glu Phe Gln Lys
305   310   315   320

Ile His Asn Glu Arg Lys Leu Asn Glu Leu Lys Glu Ile Phe Ser Phe
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Pro Arg Ile His Asp Ala Leu Pro Ile Ser Lys Glu Met Ser Lys Leu
                   340   345   350

Ser Asn Pro Lys Ile Pro Val Tyr Ile Asn Ile Cys Ser Ile Pro Ser
         355   360   365

Arg Ile Lys Gln Leu Gln Tyr Thr Ile Gly Val Leu Lys Asn Gln Cys
         370   375   380

Asp His Phe His Ile Tyr Leu Asp Gly Tyr Pro Glu Val Pro Asp Phe
385   390   395   400

Ile Lys Lys Leu Gly Asn Lys Ala Thr Val Ile Asn Cys Gln Asn Lys
                   405   410   415

Asn Glu Ser Ile Arg Asp Asn Gly Lys Phe Ile Leu Leu Glu Lys Leu
                   420   425   430

Ile Lys Glu Asn Lys Asp Gly Tyr Tyr Ile Thr Cys Asp Asp Asp Ile
         435   440   445

Arg Tyr Pro Ala Asp Tyr Ile Asn Thr Met Ile Lys Lys Ile Asn Lys
         450   455   460

Tyr Asn Asp Lys Ala Ala Ile Gly Leu His Gly Val Ile Phe Pro Ser
465   470   475   480

Arg Val Asn Lys Tyr Phe Ser Ser Asp Arg Ile Val Tyr Asn Phe Gln
              485   490   495

Lys Pro Leu Glu Asn Asp Thr Ala Val Asn Ile Leu Gly Thr Gly Thr
           500   505   510

Val Ala Phe Arg Val Ser Ile Phe Asn Lys Phe Ser Leu Ser Asp Phe
        515   520   525

Glu His Pro Gly Met Val Asp Ile Tyr Phe Ser Ile Leu Cys Lys Lys
     530   535   540

Asn Asn Ile Leu Gln Val Cys Ile Ser Arg Pro Ser Asn Trp Leu Thr
545   550   555   560

Glu Asp Asn Lys Asn Thr Glu Thr Leu Phe His Glu Phe Gln Asn Arg
              565   570   575

Asp Glu Ile Gln Ser Lys Leu Ile Ile Ser Asn Asn Pro Trp Gly Tyr
           580   585   590

Ser Ser Ile Tyr Pro Leu Leu Asn Asn Asn Ala Asn Tyr Ser Glu Leu
        595   600   605

Ile Pro Cys Leu Ser Phe Tyr Asn Glu
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tttaaaaaaa tatataccta taatcaagca ttagaagcaa agctagaaaa agataagcaa   300

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catcatgaaa gaatagaaag atgtgtaaat atattattag ctaataaaga aactattgct      720

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tattatggaa aagaaaaaat aaaaaattta ctcttgccgt tatactacaa cacaatgaga      960

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